

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2003, 23:11:13 ; Search time 579 seconds

(without alignments)

9818.681 Million cell updates/sec

Title: US-09-856-327-1

Perfect score: 2106

Sequence: 1 atgcacgatgtctctctca.....aaaaaaaaaaaaaaaaaaaaa 2106

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_19Jun03.\*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2106	100.0	2106	AAF99980	Nucleotide sequenc
2	212.4	10.1	1869	AAAC87519	Trametes hirsuta p
3	212.4	10.1	1995	AAAC87518	Trametes hirsuta p
4	208.6	9.9	1869	AAAC87420	Pyranose oxidase e
5	175.6	8.3	1902	AA246411	Pleurotus cornucop
6	152.6	7.2	1701	AAV83626	Nucleic acid encod
7	129	6.1	1946	AAA71487	T. matsutake pyran
8	129	6.1	1946	AAA07403	Trichoderma derive

9	94.4	4.5	4639	22	AA545962	Human DNA encoding
10	94.4	4.5	4640	21	AA578483	Human PRO708 (UNQ3
11	94.4	4.5	4640	25	ACA57720	Human PRO708 cDNA.
12	94.4	4.5	4640	25	ABX98190	Human cDNA encodin
13	94.4	4.5	4640	25	ABX98692	Novel human secret
14	94.4	4.5	4640	25	ACA05737	Human secreted/tra
15	94.4	4.5	4640	25	ABX97781	Human PRO polynucl
16	94.4	4.5	4640	25	ABX78565	Human PRO polynucl
17	94.4	4.5	4640	25	ABX75578	Human cDNA encodin
18	94.4	4.5	4640	25	ABX76783	Human PRO polynucl
19	94.4	4.5	4640	25	ABX16623	Human cDNA encodin
20	94.4	4.5	4649	25	ABX92359	Human cDNA encoding
21	94.4	4.5	4650	20	AAZ33987	Human PRO708 nucle
22	93.8	4.5	552	23	ABV58513	Human prostate exp
23	92.6	4.4	269	23	ABV07492	Human prostate exp
24	92.2	4.4	488	23	ABV58909	Human prostate exp
25	91.8	4.4	2440	22	AAH34932	Human colon cancer
26	91.6	4.3	485	23	ABV55622	Human prostate exp
27	91.6	4.3	2323	19	AAV59524	Human prostate exp
28	91.6	4.3	2323	24	ABV73511	Human secreted pro
29	91.4	4.3	1480	22	AA070771	Human cDNA #1 for
30	91.2	4.3	2091	24	AAAL50827	Human secreted pro
31	91.2	4.3	2710	21	AAA54132	Human cancer statu
32	91.2	4.3	2964	24	ABK70015	Breast cancer prot
33	91.2	4.3	422	23	ABV54507	cDNA encoding huma
34	90.8	4.3	1327	24	AA24775	Human prostate exp
35	90.8	4.3	1565	25	ACC00654	Glycine max ankyri
36	90.6	4.3	1992	22	AAV72748	Argemone mexicana
37	90.6	4.3	2537	25	ABV76135	Human prostate can
38	90	4.3	198	23	ABV19260	Coxsackievirus rec
39	90	4.3	400	23	ABV58615	Human prostate exp
40	90	4.3	481	23	ABV56248	Human prostate exp
41	90	4.3	579	23	ABV57511	Human prostate exp
42	89.6	4.3	374	22	AAI91055	Human polynucleoti
43	89.6	4.3	1046	24	AA563134	Human polynucleoti
44	89.6	4.3	2260	22	AAI97914	Cell death protect
45	89.6	4.3	2260	22	AAI98068	Human neuroblastom

#### ALIGNMENTS

RESULT 1  
AAF99980

ID AAF99980 standard; cDNA; 2106 BP.

XX

AC AAF99980;

XX

DT 20-JUL-2001 (first entry)

XX

DE Nucleotide sequence encoding Lyophyllum shimeji antibacterial protein.

XX

KW Fungus; antibacterial; antibiotic; plant pathogen; bacterial infection;

XX

KW Pyricularia oryzae; Rhizoctonia solani; rice pathogen; ss.

XX

OS Lyophyllum shimeji.

XX

FH Key Location/Qualifiers

XX

FT CDS

XX

FT

FT

FT

FT

FT

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FT

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FT

FT

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FT

PI Takakura Y, Kuwata S, Inoue Y;  
 DR WPI; 2001-281598/29.  
 DR P-PSDB; AAB97035.  
 XX  
 PT Antibacterial protein and encoded gene isolated from *Lyophyllum*  
 PT shimeji, with activity against plant pathogenic bacteria, applicable in  
 PT agriculture e.g. rice cultivation at low concentration, produced at low  
 PT cost on large scale  
 XX  
 PS Claim 12; Page 38-42; 52pp; Japanese.  
 XX  
 CC The present sequence encodes an antibacterial protein from the fungus  
 CC *Lyophyllum shimeji*. The protein was obtained from a fraction prepared  
 CC by extracting *Lyophyllum shimeji* with water and subjecting the extract  
 CC to ammonium sulphate precipitation. The protein inhibits the growth  
 CC of the plant pathogenic bacteria *Pyricularia oryzae* and *Rhizoctonia*  
 CC solani at a relatively low concentration. P. oryzae and R. solani are  
 CC causative of the two major diseases of rice. The protein contains  
 CC components of 70 kDa and 65 kDa, as determined by SDS-PAGE.  
 CC The antibacterial protein can be produced at low cost on a large scale.  
 XX  
 SQ Sequence 2106 BP; 593 A; 540 C; 527 G; 446 T; 0 other;  
 Query Match 100.0%; Score 2106; DB 22; Length 2106;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATCAGCCATGCTCTCTCAACGAGCAGATGCTACGCGACTATCCACGCTCTATCAAAAT 60  
 DB 1 ATCAGCCATGCTCTCTCAACGAGCAGATGCTACGCGACTATCCACGCTCTATCAAAAT 60  
 QY 61 CAACGAGCAGATTCCTAAGACGCAATTCAGCAACATACGGAACGAGGATGTATGT 120  
 DB 61 CAACGAGCAGATTCCTAAGACGCAATTCAGCAACATACGGAACGAGGATGTATGT 120  
 QY 121 ATTCATTCAGGATCTGACCCATTGGAGCGACGATGATCAAGCTCTGTTGAAGCTGG 180  
 DB 121 ATTCATTCAGGATCTGACCCATTGGAGCGACGATGATCAAGCTCTGTTGAAGCTGG 180  
 QY 181 TCTAGCTGTTGATGTCGAGATCGGAGCTGCTGATAGCTTCTACGCTGTTAATGCCGA 240  
 DB 181 TCTAGCTGTTGATGTCGAGATCGGAGCTGCTGATAGCTTCTACGCTGTTAATGCCGA 240  
 QY 241 AGAAGGAATCTGATTCCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 DB 241 AGAAGGAATCTGATTCCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 QY 301 GAAAGATATTGACCGCTTCGTCATGTAATCAAGGAGCCCTTCAACAAGTCTCTGTTC 360  
 DB 301 GAAAGATATTGACCGCTTCGTCATGTAATCAAGGAGCCCTTCAACAAGTCTCTGTTC 360  
 QY 361 TGTGAGAAACAGAACGTCGCTACACTTGGATCCGAGCGCTGGAGCGCGCCCTGGAAG 420  
 DB 361 TGTGAGAAACAGAACGTCGCTACACTTGGATCCGAGCGCTGGAGCGCGCCCTGGAAG 420  
 QY 421 TTCAGCCATATCGAACGGTAAATCTCACCAGCGGGAATTCGAGAACTTGTTCGCGGA 480  
 DB 421 TTCAGCCATATCGAACGGTAAATCTCACCAGCGGGAATTCGAGAACTTGTTCGCGGA 480  
 QY 481 GGCGGTAAACGGTGGAGTCGGCGCATGAGTACCCACTGGACGTGCTCCACGCGGAT 540  
 DB 481 GGCGGTAAACGGTGGAGTCGGCGCATGAGTACCCACTGGACGTGCTCCACGCGGAT 540  
 QY 541 TCATCCACCCATGGAAGTCTCCGGGCATCGCGCGCTCCGAAGCTCAGTAACGACCCGGC 600  
 DB 541 TCATCCACCCATGGAAGTCTCCGGGCATCGCGCGCTCCGAAGCTCAGTAACGACCCGGC 600  
 QY 601 AGAGGAGCAAAAGAGTGGAAACGAGCTTTATCCGAGCGCGAGCGTCTCATCGGGACTTC 660  
 DB 601 AGAGGAGCAAAAGAGTGGAAACGAGCTTTATCCGAGCGCGAGCGTCTCATCGGGACTTC 660  
 QY 661 CACCAAGGAATTCGACGAGTCAATTCGGGCACACCCCTTTGTCGCGCTCTTTGCAAGACGC 720

DB 661 CACCAAGGAATTCGACGAGTCAATTCGGCACACCCCTGTTCTCGGCTCTTTGCAAGACGC 720  
 QY 721 GTACAGGATCGTCAACGATCTTTTCCGCTCTCCGTTGGCATGGCACCGTGAAGAA 780  
 DB 721 GTACAGGATCGTCAACGATCTTTTCCGCTCTCCGTTGGCATGGCACCGTGAAGAA 780  
 QY 781 CGCGCGGGAATACGTCGAATGGCAGTACGAGAAATCTTTTCCACTCTATCTACACGA 840  
 DB 781 CGCGCGGGAATACGTCGAATGGCAGTACGAGAAATCTTTTCCACTCTATCTACACGA 840  
 QY 841 TGACAAGCAGAAAGAGCTCTTTTACCCTGCTGAGAAACCATCGCTGCACAGACTGGCGCT 900  
 DB 841 TGACAAGCAGAAAGAGCTCTTTTACCCTGCTGAGAAACCATCGCTGCACAGACTGGCGCT 900  
 QY 901 TACGGCGGGTATGAGAAAGATTTGGCGCTGCCGAGGTGAGGAATCTACTGGCCACCAG 960  
 DB 901 TACGGCGGGTATGAGAAAGATTTGGCGCTGCCGAGGTGAGGAATCTACTGGCCACCAG 960  
 QY 961 GAATCCTAGTTCCGAGCTGACAGCTATATCATGCGGAAGGTATATGTACTGCGCTCGG 1020  
 DB 961 GAATCCTAGTTCCGAGCTGACAGCTATATCATGCGGAAGGTATATGTACTGCGCTCGG 1020  
 QY 1021 AGCGATCGGCAACCCACAGATTTCTTAACTCGGGCTTCTCTGGGCTACAGTCAAGCC 1080  
 DB 1021 AGCGATCGGCAACCCACAGATTTCTTAACTCGGGCTTCTCTGGGCTACAGTCAAGCC 1080  
 QY 1081 ACGCAATGACCTGTTGATCCCAACCTGGGAGGTACATCAGCGAGCAGCCGATGCAAT 1140  
 DB 1081 ACGCAATGACCTGTTGATCCCAACCTGGGAGGTACATCAGCGAGCAGCCGATGCAAT 1140  
 QY 1141 TTGCCAGATAGTCTTTGAGCGAGGAATTCGTCACAGCGTGGCGAGGTATCTTATGGACT 1200  
 DB 1141 TTGCCAGATAGTCTTTGAGCGAGGAATTCGTCACAGCGTGGCGAGGTATCTTATGGACT 1200  
 QY 1201 GCCATGTTGGAAGAGCCGTTGCTCAACATATTCGCAAGAACCCGACAGATGCACTGCC 1260  
 DB 1201 GCCATGTTGGAAGAGCCGTTGCTCAACATATTCGCAAGAACCCGACAGATGCACTGCC 1260  
 QY 1261 CATTCGTTCCGCGATCCGAGCAACCCAGGTACACACCCATTTACAGAAACACCCCTG 1320  
 DB 1261 CATTCGTTCCGCGATCCGAGCAACCCAGGTACACACCCATTTACAGAAACACCCCTG 1320  
 QY 1321 GCACACGAGATTCACCGCGATGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 DB 1321 GCACACGAGATTCACCGCGATGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 QY 1381 TCGTGTATCGTTCGACCTGCGCTGCTTTGGCGCAACCCGACCTTGAAGCAACACCTTTT 1440  
 DB 1381 TCGTGTATCGTTCGACCTGCGCTGCTTTGGCGCAACCCGACCTTGAAGCAACACCTTTT 1440  
 QY 1441 GGTTCCTCAGACGATGTTCAAGACGGGTACAGTATGCCGAGCGGAGGTTTCAGATATCG 1500  
 DB 1441 GGTTCCTCAGACGATGTTCAAGACGGGTACAGTATGCCGAGCGGAGGTTTCAGATATCG 1500  
 QY 1501 ACCCAGACCTGCGTCAAAACGTCGAGCAAGGAAATGATGCCCATATGTCGGAAGTGGC 1560  
 DB 1501 ACCCAGACCTGCGTCAAAACGTCGAGCAAGGAAATGATGCCCATATGTCGGAAGTGGC 1560  
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 DB 1561 GAGCAACTTGGGAGGTTATTTGCCACGTCCTCCCGCCAGTATTTATGATCCAGGCTTGC 1620  
 QY 1621 ACTTCATCTTGGGAGGTTATTTGCCACGTCCTCCCGCCAGTATTTATGATCCAGGCTTGC 1680  
 DB 1621 ACTTCATCTTGGGAGGTTATTTGCCACGTCCTCCCGCCAGTATTTATGATCCAGGCTTGC 1680  
 QY 1681 CAACTCGTGTCTGGGACTTTCGCAATCTTTTATGTTGAGGCAATACAGTGTGCTGATAA 1740  
 DB 1681 CAACTCGTGTCTGGGACTTTCGCAATCTTTTATGTTGAGGCAATACAGTGTGCTGATAA 1740  
 QY 1741 GGCGTTCGCGAGAACCCGACACTTACGTCGATGTCGCGCTATCAAGAGCCGAGGAG 1800

Db 1741 GGGCTTCGGCGAGAACCGACACTTACGTCGATGTGCCACGCTATCAAGAGCGCGAGGAG 1800  
 Qy 1801 CATCATCAATCACTCAAGGTGGGACTGACGGAAAAATACAGCGGAGCATCGCAACCT 1860  
 Db 1801 CATCATCAATCACTCAAGGTGGGACTGACGGAAAAATACAGCGGAGCATCGCAACCT 1860  
 Qy 1861 TTGAGGAGGAGCAACAGCAGCTGTAAACAAACCGGCTCAAGTGGCTACTTCAAGTTGAATG 1920  
 Db 1861 TTGAGGAGGAGCAACAGCAGCTGTAAACAAACCGGCTCAAGTGGCTACTTCAAGTTGAATG 1920  
 Qy 1921 CATCTGCTCCCTACCATGTTGATGTGTACGATAGGCTGTGAAGATTGTGTATPAC 1980  
 Db 1921 CATCTGCTCCCTACCATGTTGATGTGTACGATAGGCTGTGAAGATTGTGTATPAC 1980  
 Qy 1981 TGAACCTGTACTTGTCTGATAGTATGTCACATGATGTCATGTTTAAAAAATAAAAA 2040  
 Db 1981 TGAACCTGTACTTGTCTGATAGTATGTCACATGATGTCATGTTTAAAAAATAAAAA 2040  
 Qy 2041 AAA 2100  
 Db 2041 AAA 2100  
 Qy 2101 AAAAAA 2106  
 Db 2101 AAAAAA 2106

## RESULT 2

AAC87519

ID AAC87519 standard; DNA; 1869 BP.

XX AC

AAC87519;

XX 13-MAR-2001 (first entry)

XX DE

XX Trametes hirsuta pyranose oxidase cDNA, SEQ ID NO:1 (version 2).

XX Pyranose oxidase; expression construct; recombinant production;

XX monosaccharide oxidation; 2-keto derivative;

XX hydrogen peroxide production; ss.

XX OS

XX Trametes hirsuta.

XX US6146865-A.

XX PN

XX 14-NOV-2000.

XX PD

XX 05-MAY-1999; 99US-0305381.

XX PF

XX 08-JUN-1998; 98DK-0000774.

XX PR

XX 10-JUN-1998; 98US-0088724.

XX XX

XX PA (NOVO ) NOVO NORDISK AS.

XX XX

XX PI Schneider P, Christensen S, Lassen SF;

XX XX

XX WPI: 2001-049055/06.

XX DR P-PSDB; AAB48832.

XX XX

PT Novel nucleic acid molecule encoding polypeptide having pyranose  
 PT oxidase activity used to design oligonucleotide probes to identify and  
 PT clone DNA encoding the polypeptide from different genera or species -

XX XX

XX Claim 2; Column 25-28; 20pp; English.

XX XX

XX The invention relates to nucleic acids (e.g., AAC87518, AAC87519) which  
 CC encode Trametes hirsuta pyranose oxidase (AAB48832). The invention also  
 CC relates to expression constructs, expression vectors and recombinant  
 CC cells comprising pyranose oxidase nucleic acid sequences, and the  
 CC recombinant production of Trametes hirsuta pyranose oxidase. Pyranose  
 CC oxidase catalyses the oxidation of several monosaccharides in the  
 CC pyranose form at position C2 to produce 2-keto derivatives with the  
 CC release of hydrogen peroxide. Nucleic acids encoding Trametes hirsuta

CC pyranose oxidase may be used to produce the enzyme and to design  
 CC oligonucleotide probes to identify and clone genomic pyranose oxidase  
 CC cDNA or genomic DNA from different genera or species of microorganisms  
 CC (fungi or bacteria). The present sequence represents a cDNA encoding  
 CC pyranose oxidase from the fungus Trametes hirsuta.  
 CC Note: Both AAC87518 and AAC87519 are Trametes hirsuta pyranose oxidase  
 CC cDNA sequences which contain the entire open reading frame (ORF).  
 CC However, the two sequences have different stop codons - AAC87518 has an  
 CC opal stop codon while AAC87519 has an amber stop codon.  
 XX

SQ Sequence 1869 BP; 397 A; 622 C; 548 G; 302 T; 0 other;

Query Match 10.1%; Score 212.4; DB 22; Length 1869;

Best Local Similarity 51.5%; Pred. No. 3.2e-25;

Matches 841; Conservative 0; Mismatches 656; Indels 135; Gaps 10;

Qy 269 GGCTACCACAAAGAAGATGAATCGAGTTCACAGAAGATATGACCGCTTCGTCATGTA 328

Db 259 GGCTACACAAAGAAGACACCGTCGAGTACCAGAAGAACATCGACAAATTCGTAATGTT 318

Qy 329 ATCAAGGGAGGCTTACACAAAGTCTCTGTTCTCTCAGAACACAGACGTCCTACACTT 388

Db 319 ATCAAGGGCAACTTATGCCGCTCTCGGTGCCGCTCAACAGATGTCGTTGACACGCTA 378

Qy 389 GATCCCGGAGCTGCGCGCCCTTGGAAAGTTTCAGCATATCGAAGGTAAAAATCCT 448

Db 379 AGCCCGGCTCATGCAAGCTTCGACG-----TCTTCGTCGCCAACGGGCGCAATCCA 432

Qy 449 CACCAGCGGGAATTCGAGAACTTCTCGCGGAGCGCTTAACGCTGGAGTCGGCGGCATG 508

Db 433 GAGCAAGACCGCTGCGCAACCTTAGTGGCCAGGCGGTCAACCGCTGCTGGCGGCATG 492

Qy 509 AGTACCACATGAGCGTCTCACGCCACGAGTTCATCCACCATGGAAGATCTCCCGGCG 568

Db 493 TCTACGCACTGGAGCTGCGCGACGCGCGCTTCGAGAAGCTGCAG----- 537

Qy 569 ATCGCGCTGCGGAAGCTCAGTAACGACCGCGCAGGACGACAAAGATGGAACGAGCTT 628

Db 538 ---CGCCCGCTGCTGCTGTAAGAACGACTCAAGCGGACGACGCGGAGTGGGACGAGCTC 594

Qy 629 TATTCGAGGCGGAGCGTCTCTATCGGAGCTTCCACCAAGGAATTCGACGAGTCAATTCGG 688

Db 595 TACAAGAAAGCGGAGTCTACTTCAAGACCGGACGACGCCAGTTCGCGGAGTCGATCCGC 654

Qy 689 CACACCTTGTTCGCGCTCTTTCGAAGACGCGTACAAAGATGCTCAACGATATCTTCGCG 748

Db 655 CACAACCTCGTCTCAAGAAGCTGACAGGAGGAGTACAAG---GCGTGCAGCTTCCAG 711

Qy 749 CCTCTCCGCTTGGCATGCCACCGGTTGAAGAAGCGCGGAAATACGTCGAATGCACTCA 808

Db 712 CAGATCCCGCTCGCGGCGACGCGCAGA-----GCCCGAGTTCGTCGAGTGGAGTCG 765

Qy 809 GCAGAAATCTTTTCCACTCTATCTACACGATGACAAAGCAGAGAGAGCTCTTTTACCCCTG 868

Db 766 GCGCACACCGTGTT-----CGATCTCGAAGAACCGGCGCAACAGGACGCG 810

Qy 869 CTGACGAACCATCGCTCCACAGCACTGGCGCTTACGGCGGGGTATGAGAAGAGATTGGC 928

Db 811 CCGAAGCAGCGCTTCAACCTCTTCCCGCGCTGCGGTGCACGAACGCTGAGCGCGGATAAC 870

Qy 929 GCTGCCGAGTCAAGGAATCTACTGGCCACGAGGAATCTAGTTCGACGCTGGACAGCTAT 988

Db 871 GCGAATCGGAGATGCTAGGCGCTGATGTCGCGGACCTCCACGCGGCGCAAGACATCAC 930

Qy 989 ATCATGCGGAAGGTATATGTACTGGCTCGGAGCGGATCGGCAACCCACAGATCTCTAT 1048

Db 931 ATCAAGGCCAAGGTGTACATCTCTACCGCGCGCGGTCTCCACAACGCGCAGCTCTCGCG 990

Qy 1049 AACTCGGGCTT-----CTCTGGGTACAGGTTCACGCCACCAATGAC--TCGTTGATC 1099

Db 991 GCCTCTGGATTGCGGCGAGCTGGTCTGCTCCGACCCCGCAAGCGCTGCTGCTGCTGCTG 1050

Qy 1100 CCCAACCTGGGAGGTACATCACGGAGCAGCCCGATGGCATTTTGGCAGATAGTCTTGAGG 1159

Db 1051 CCGTACCTGGGACCCACATCACCGAGCAGCGCTGCTCTTCTGCCAGCCTCATGAC 1110  
 QY 1160 CAGGAATTCGTGCACAGCGTGGCGACGATC----- 1190  
 Db 1111 ACGGAGCTCATCAACAGTGTCCCGCGGATATGACCAATGTGGCAAGCCCGGCCACCG 1170  
 QY 1191 -----CTTATGGACTGCCATGGTGGAAA 1213  
 Db 1171 GACTATAGCGTCACGTATACCCCGGCGACCGACACAGACACCGGACTGGTGGAC 1230  
 QY 1214 GAAGCGGTGTCACATATGCCAAGAACCGCAGATGCACCTGCCATTCGTTCCGC 1273  
 Db 1231 GAGAAGGTGAAGAAGCACATGATGGACCAACAGGAGGACCGCTCCCGATCCGTTCCGAG 1290  
 QY 1274 GATCGGGAACCCAGGTACACACCCCATTTACAGAGACACCCCTGGCAGCAGATTT 1333  
 Db 1291 GACCTGAGCCGCGAGTACCACGCTGTTTCAGGCAACGCCACCCATGGCACACCCAGATT 1350  
 QY 1334 CACCGCGATGCTTTTTCGTACGTCGCTCGGTCCTGAGGTGGACTCTGTCATCGTC 1393  
 Db 1351 CACCGCGAGCGCTTCAGCTACGCGCGCTGCGACGAGCATGCTCGGGCTCATGCTC 1410  
 QY 1394 GACCTGCGGTGTTGGCGCAACCGACCGCTGAAGCAACAACTTTTGGTTTCCAGAAC 1453  
 Db 1411 GACTGGCGGTCTTCGGACGCGACCGACCGGCGCAAGGAGGAGAACTATGTTCTCGGAC 1470  
 QY 1454 GATGTTCAAGCGGTGACATGTCGCGAGCGGAGTTCAGATATCGACCCAGCAGCTCG 1513  
 Db 1471 AGATCAGGAGCGGTACACCTCCGCGAGCGCGAGTTCGAGCTTCGCTTCCCGGGG-- 1528  
 QY 1514 TCAAACGTGAGAGGAAGAAATATGTCGCGATATGTGCGAAGTGGCGAGCAACTTGGGA 1573  
 Db 1529 -----GCCGGAAGCGGAGGACATGATGACCGACATGTCGGTATGTCGCGGAGATCGGT 1584  
 QY 1574 GGTATTTGCCAGCTCCCGCCGAGTTTATGGATCCAGCGCTTGCATCTTCATCTTCG 1633  
 Db 1585 GATTCCTCGCTGGGTCTTACCCACAGTTCATGGAGCCCGGCTTGTCTGCTGACCTTGT 1644  
 QY 1634 GGGACTACTCGCATTTGGCTTCGACAA-----GGCACTACAGTGGCTGATACACATCG 1687  
 Db 1645 GGGAGCACCGCATGGGTTTCGACGAGAAGCGGCAAGTCTGGGTGACACCGACTCA 1704  
 QY 1688 CTGGTCTGGGATTTGCAATCTTTATGTCAGGCAATGGCAACCATCAGGACGGGCTTC 1747  
 Db 1705 CGCGTCTCGGCTTCAAGAACTCTTCTCGCGGCTGCGGGAACATCCCAACCGGCTAC 1764  
 QY 1748 GCGGGAACCCGACACTTACGTGATGTCGACGCTATCAAGAGCGGAGGAGCATATC 1807  
 Db 1765 GCCGGAACCCGAGCTCACCGCAATGTGCTTGGATCAAGAGCTGCGAGTACATCAAG 1824  
 QY 1808 AATACATCAAG 1819  
 Db 1825 AAGAACTTCGAG 1836

## RESULT 3

AAC87518

ID AAC87518 standard; DNA; 1995 BP.

XX AAC87518;

AC AAC87518;

DT 13-MAR-2001 (first entry)

XX Trametes hirsuta pyranose oxidase cDNA, SEQ ID NO:1 (version 1).

DE Pyranose oxidase; expression construct; recombinant production;

KW monosaccharide oxidation; 2-keto derivative;

XX hydrogen peroxide production; ss.

OS Trametes hirsuta.

XX US6146865-A.

PN

XX 14-NOV-2000.  
 PD 05-MAY-1999; 99US-0305381.  
 XX 08-JUN-1998; 98DK-0000774.  
 PR 10-JUN-1998; 98US-0088724.  
 XX (NOVO ) NOVO NORDISK AS.  
 PA  
 XX  
 PI Schneider P, Christensen S, Lassen SF;  
 XX WPI: 2001-049055/06.  
 DR P-PSDB; AAB48832.

XX Novel nucleic acid molecule encoding polypeptide having pyranose  
 PT oxidase activity used to design oligonucleotide probes to identify and  
 PT clone DNA encoding the polypeptide from different genera or species -  
 XX Claim 2; Fig 1; 20pp; English.

XX The invention relates to nucleic acids (e.g., AAC87518, AAC87519) which  
 CC encode Trametes hirsuta pyranose oxidase (AAB48832). The invention also  
 CC relates to expression constructs, expression vectors and recombinant  
 CC cells comprising pyranose oxidase nucleic acid sequences, and the  
 CC recombinant production of Trametes hirsuta pyranose oxidase. Pyranose  
 CC oxidase catalyses the oxidation of several monosaccharides in the  
 CC pyranose form at position C2 to produce 2-keto derivatives with the  
 CC release of hydrogen peroxide. Nucleic acids encoding Trametes hirsuta  
 CC pyranose oxidase may be used to produce the enzyme and to design  
 CC oligonucleotide probes to identify and clone genomic pyranose oxidase  
 CC cDNA or genomic DNA from different genera or species of microorganisms  
 CC (fungi or bacteria). The present sequence represents a cDNA encoding  
 CC pyranose oxidase from the fungus Trametes hirsuta.

CC Note: Both AAC87518 and AAC87519 are Trametes hirsuta pyranose oxidase  
 CC cDNA sequences which contain the entire open reading frame (ORF).  
 CC However, the two sequences have different stop codons - AAC87518 has an  
 CC opal stop codon while AAC87519 has an amber stop codon.  
 XX Sequence 1995 BP; 437 A; 649 C; 574 G; 335 T; 0 other;

Query Match 10.1%; Score 212.4; DB 22; Length 1995;  
 Best Local Similarity 51.1%; Pred. No. 3.2e-25;  
 Matches 841; Conservative 0; Mismatches 656; Indels 135; Gaps 10;

QY 269 GCCTACACACAGAGAAATGAATCGAGTTCGAGAAGATATTGACCGTTCGCTCAATGTA 328  
 Db 288 GGCCTACACAAAGAGAACACCGTTCGAGTACCAGAAACATCGACAAATTCGTAATGTT 347  
 QY 329 ATCAAGGGAGCCTTACACAAAGTCTCTGTTCTGTGTCAGAACACGAGCTGCTACACTT 388  
 Db 348 ATACAGGGCAACTATGTCCTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 407  
 QY 389 GATCCCGGAGCTGAGCGGCCCGCTGGAAGTTCAGCCATATCAAGCGTAAATACCT 448  
 Db 408 AGCCCGGCTCATGCGAGCTTCGACG-----TCTCTGTCGCGAAGCGGCGGATCCA 461  
 QY 449 CACGAGCGGGAATTCGAGAACTTGTCTCGGAGCGCGTAAACGCTGGAGTCGCGCGCATG 508  
 Db 462 GAGCAAGACCGGCTGCGCAACCTTAGTGGCCACCGGGTCAACCGGCTGCTGCGCGCATG 521  
 QY 509 AGTACCCACTGGAGCTGCTCCACCGCCAGGATTCATCCACCCATGGAAGTCTCCCGGGC 568  
 Db 522 TCTACGCACTGGAGCTGCGCGACCGCGCTTCGAGAAGCTGTCAG----- 566  
 QY 569 ATCGGCGCTCGGAAGCTCAGTAACGACCGCGCAGGACGACAAAGAGTGAACGAGCTT 628  
 Db 567 ---CGCCCGCTGCTCGTGAAGAACGACTCCNAGCGGAGACGCGCGGAGTGGAGCAGGCTC 623  
 QY 629 TATTCGAGCGCGAGCGCTCTCATCGGACTTCCACCAAGGAATTCGACGAGTCAATTCGG 688  
 Db 624 TACAAGAGCCGAGTCTGTTACTTCAAGACCGGACGACCCAGTTCGCGGAGTCTGATCCGC 683

QY	689	CACACCCCTTGTTCGGCGCTCTTTGCAAGACCGGTACAAAGGATCGTCAACGSTATCTTTTCG	748
DB	684	CACAACTCGTGCCTCAAGAACTCGAGGAGAGTACAAG---GCGTGGCGACTTCACG	740
QY	749	CCTCTCCGTTGGCATGCCACCGGTTGAAGAACCGCGGGATACGTCGATGCGACTCA	808
DB	741	CAGATCCGCTCGGGGACGCGCCAGA-----GCCCGAGCTTCGTCGAGTGGAGCTCG	794
QY	809	GCAGAAATCTTTTCCACTCTATCTACAACGATGACAAGCAAGAAAGCTCTTTTACCCTG	868
DB	795	GCGCACACCCGGTT-----CGATCTCGAGACCGCGCGCAACGAGACGCG	839
QY	869	CTGACGAACCATCGCTGCACAGACTGGCGCTTACGGGCGGGTATGAGAAGAAGATTGGC	928
DB	840	CCGAAGCAGCGCTTCAACCTCTTCCCGCGCTCGCTGCACGAACGCTGAGCGCGATAAC	899
QY	929	GCTCCGAGGTCAAGAACTACTTCTGGCCACACAGGAATCCTAGTTCGCGAGCTGGACAGCTAT	988
DB	900	GCGAACTCGGATCTGTAGGCTCGATGTCGCGACCTCCACGGGGGCAAGAGCATCACC	959
QY	989	ATCATGCGAAGGATATGTACTGGCGTCGGGAGCGATCGGCAACCCACACAGATTCTCTAT	1048
DB	960	ATCAAGCCCAAGGTGTACATCTTCAACCGCGCGCGGTCCACACGCGCAGCTCTCGCG	1019
QY	1049	AACTCGGGCTT-----CTCTGGGCTACAGGTACGCCACGCAATGAC--TGCTTGATC	1099
DB	1020	GCCTCTGGATTGGGCGACCTGGGTCTGCGGACCCCGCCCAAGCGCTCGCTCTCTGCTG	1079
QY	1100	CCCAACCTGGGAGGTACATCACGGACACCGNATGCATTTTCCAGATAGTCTTGAGG	1159
DB	1080	CCGTACTCTGGGACCCACATCACCGACGACGCTGCTCTTCTGCCAGCCGTCATGAGC	1139
QY	1160	CAGGAATCTGCACACGCTGGCGGAGATC-----	1190
DB	1140	ACGGAGCTCATCAACAGTGTCAACCGGGATATGACCATTTCGCGCAAGCCCGCCACCG	1199
QY	1191	-----CTTATGAGCTGCCATGGTGAAA	1213
DB	1200	GACTATAGCTACGTATATCCCGGGCAACCCGAAACAAGCACCGGACTGGTGAAC	1259
QY	1214	GAAGCCCTTGTCAACATATTGCCAAGACCCGACAGATGCACTGCCATTCGTTCCCGC	1273
DB	1260	GAGNAGTGGAAGACATGATGGACCACGAGGAGCCGCTCCCGATCCCGTTTCGGAG	1319
QY	1274	GATCCGGAACCCAGGTAAACCCCATTTACAGAAGAACCCCTGGCACACGCAAGATT	1333
DB	1320	GACCTGAGCGCAGGTCAACACGCTGTTTCAGGCAACGACCCATCGGCACACCCAGATT	1379
QY	1334	CACCGCGATGCTTTTGGTAGGTGCGTTCGCTCTGAGGTGGAATCTCGTGTCACTGTC	1393
DB	1380	CACCGGACGCTTACGATACGCGCGCGTGCACGAGAGCATCGACGCGGCTCATCGTC	1439
QY	1394	GACCTGCGCTGTTTGGCGCAACCGACCTGAAACAACACCTTTTGGTTTTCAGAAC	1453
DB	1440	GATGCGGTTCTTCGGACGACCCGAGCCCAAGGAGGAACAAGATATGGTTCTCGGAC	1499
QY	1454	GATGTTCAAGACGGGTACAGTATGCGCGACGCCACGTTTACAGATATGACCCACACTGCG	1513
DB	1500	AAGATCAGGACCGGTACAACCTTCGGCAGCCGACCGTTCGACTTCGCTTCCCGGGG--	1557
QY	1514	TCAAACGTGAGACAAGGAAATGATGGCCGATATGTGCGAAGTGGCGAGCAACTTGGGA	1573
DB	1558	-----GCCCGCAAGCGGAGCATGATGACCGACATGTGGTCTATGTGCGGGAAGATCGGT	1613
QY	1574	GGTATTTCGCCAGCTTCCCCCGCAGTTTATGGATCCAGGCCCTTGCATCTCATCTTGGG	1633
DB	1614	GGATTCTGCTGGGTCTTACCACAGTTTCATGGAGCCCGGCTTGTCTCTGCACCTTGT	1673
QY	1634	GGGACTACTCGCATTTGGCTTCGACAA-----GGCAACTACAGTGGCTGATACAACCTCG	1687
DB	1674	GGGACCGCCGATGGCTTCGACGAGAGAGGGGACAAAGTGTGGCTCGACCCGACTCA	1733
QY	1688	CTGGCTGGGACTTTGCCAATCTTTATGTTGCAAGCAATGGACCAATCAGGACGGGCTTC	1747

Db	1734	CGCGTCTTCGGCTTCAGAGACCTCTCC	TGGCGGCGCTGCGGGAACATCC	CCACCGCGTAC	1793
QY	1748	GCGGAGAACCGCACACTTACGTCGATGTGCC	CACGCTATCAAGAGCGGAGGAGCATCATC		1807
Db	1794	GCCGCGAACCGGAGCGCTCACCGCAATGT	CGCTTCGGATCAAGAGCTCGGAGTACATCAAG		1853
QY	1808	AATACACTCAAG	1819		
Db	1854	AAGAACTTCGAG	1865		

## RESULT 4

RECEIVED  
AAT34420  
ID AAT34420 standard; cDNA; 1869 BP.

XX AAT34420:

27-NOV-1996 (first entry)

Pyranose oxidase encoding sequence.

Pyranose oxidase; glucose; oxidation; glucanose; assay; diabetes;  
KW  
marker; diagnosis; 1,5-anhydro-D-sorbitol; ss.  
KW

OS Coriolus versicolor.

PN DE19545780-A1.

13-JUN-1996

PF 07-DEC-1995; 95DE-1045780.

PR 24-MAY-1995; 95JP-0124835.

[illegible]

XX  
XX

PI Suzuki M;  
Kawar S; Kojima I; Minamimura I; Nishimura I; Oryama K;

DR WPI; 1996

[illegible]

PT 1,5-anhydro-D-sorbitol used as marker for diabetes diagnosis

PS Claim 1; Page 10-13; 22pp; German.

CC The present sequence encodes a protein isolated from *Coriobacterium versicolor*,  
CC which has the enzyme activity of pyruvate oxidase (PO). The PO oxidises  
CC glucose to gluconone and has an optimum pH of 7-7.5. It has a mol. wt. of  
CC 230000 (determined by gel filtration) and is stable at around 50deg.C.  
CC PO can be used for measurement of glucose in, e.g. foods or body fluids,  
CC or 1,5-anhydro-D-sorbitol which is an important marker used in the  
CC diagnosis of diabetes.

Sequence 1869 BP; 408 A; 601 C; 521 G; 339 T; 0 other;

Query Match 9.98; Score 208.6; DB 17; Length 1869;

Best local similarity 50.4%; Pseud. NO. 1.3E-24;  
Matches 856; Conservative 0; Mismatches 714; Indels 129; Gaps 9

QY 200 GAGATCGGAGCTGCTGATAGCTTCTACGCTGTTAATGCCGAAGAAGGAAGTGCAGTTCCC 259

Db 190. GAGCTCGTGAAGCCGGTTACAAGGTCGCCATGTTTCGACATCGGGAAATTGACTCTGGC 249

QY 260 TACGTTCTGGCTACCAAGAAGATGAAATCGAGTTCAGAAAGATATTGACCGCTTC 319

Db 250 CTGAAGATCGGTGCCCAAGAAGAACACCGTCGAATACCAGAAGAACATTGACAAAGTTT 309

QY 320 GTCAATGTAATCAAGGGAGCCTTACAACAAGTCTCTGTTCCCTGTCAGAAACCAGAACGTG 379

Db 310 GTGAAGCTATTACGGCCCAATTGATGCTGTGTTCCGTTCCGTCATACCCCTCGTGATC 369  
QY 380 CCTACACTTGTATCCCGGAGCGTGAGCGCGCCGCCCTGGAAAGTTTACGCCATATGAACGGT 439  
Db 370 GACACGCTAGCCCGGAGCTGTGCAAGCTTCATCG -----TTCCTCGTCCGCAATGGC 423  
QY 440 AAAAATCCTCACCAGCGGGAATTCGAGAACTTCTTCGCGAGGCGGTAAAGCGGTGAGTC 499  
Db 424 TCGNACCCAGACAGACCGCGTTCTGTAACCTCAGTGGTCAGCGGCTCAGCGGTGTCGTC 483  
QY 500 GGGCGCATAGTACCCACTGAGCGTCTCCACGCCACGGATTATCCACCCATGGAAGT 559  
Db 484 GGAGGCATGTCCACGCACTGGACATCGCGACACCGCGCTTGA ----- 527  
QY 560 CTCGCCGATCGCGCTCGGAAGCTCAGTAACGACCGCGCAGAGGACGACAAAGAGTGG 619  
Db 528 --CCGGAGCAGCGCCCGTTGCTCGTGAAGGAGCAGCAGGACGCTGACGACGCGAGTGG 585  
QY 620 AACGAGCTTATTCCGAGCGCGAGCGTCTCATCGGACTTCCACCAAGGAAATTCGACGAG 679  
Db 586 GACCGCTGTACACCAAGCGCGAGTCTACTTCAAGACCGGACGACGACGTTTCAAGGAG 645  
QY 680 TCAATTGGCACACCTTGTTCGCTCTTTGCAAGACGCGGTACAAAGGATCGTCAACGT 739  
Db 646 TCGATCGGCACAACTCTGCTCAACAGCTCGCGGAGGAAATACAAAGTCAAGCGGAC 705  
QY 740 ATCTTTGCCCTCTCCGTTGGATGCCACCGGTTGAAGACGCGCGGAAATACGTCGAA 799  
Db 706 TTCCAGCAGATCCCCCTCGCGCAACGCTCG -----CAGTCCGACCTTCGTCGAG 756  
QY 800 TGGCACTCAGCAGAAATCTTTTCCACTTATCTACACGATGACAAAGCAAGAGAGCTC 859  
Db 757 TGGAGCTCGGCAACACCGTGT -----CGACCTCCAGAACAGGCGCGAAC 801  
QY 860 TTATCCCTGCTCAGCAACCATCGCTGCACACGACTGGCGCTTACGGCGGGTATGAGAAG 919  
Db 802 ACGGACGCGCGCAATGAGCGCTTCAACCTCTTCCCGCGGTTCATGTGAGCGGCTG 861  
QY 920 AAGATTGGCGTTCGCGAGTCAGGAATCTACTGGCCACAGGAATCTTAGTTCGAGCTG 979  
Db 862 CCACACAGCTGCAATCCGAGATCGAGAGTGTGCACATCCACGACCTCATCTCCGCGAC 921  
QY 980 GACAGCTATATCATGCGAAGGTATATGTACTGGCGTGGGAGCGATCGGCAACCCACAG 1039  
Db 922 CGCTTCGAAATCAGACAGACGTGTGCTTCTTACAGCGGGCGGTCCACAAACGCGGAG 981  
QY 1040 ATTCTCTATACTCGGGT -----CTCTGGGCTACAGGTCAACGCCACGCAATGACTCG 1093  
Db 982 CTTCCTGTGAACCTCTGGCTTGGACAGCTGGGCGCGCGACCCCGCGAACCCGCGCAG 1041  
QY 1094 TTGATCCCAACCTGGGAGGTACATCAGGAGCAGCGATGGCATTTTGGCAGATAGTC 1153  
Db 1042 TTGCTGCCGTCCCTCGAAGCTACATCACCAGCAGTCTGCTCTTCTGCGACAGCGTG 1101  
QY 1154 TTGAGCGAGGAATTCGTGACAGCGTG -----CGGACGATCCTTATGACTGCC ----- 1203  
Db 1102 ATGACCCGAGCTCATCGACAGCTGAAGTCCGACATGATCATCAGGGGCAACCTGGC 1161  
QY 1204 -----ATGG 1207  
Db 1162 GATCTGGGTTACAGGTCACGTACAGCGCGCGGAGACCAACAGCCCGGACTGG 1221  
QY 1208 TGGAAAGNAGCGGTGCTCAACATATTGCCAAGAACCGGACAGATGCACTGCCATTCCG 1267  
Db 1222 TGGAAACGAAAGGTGAAGAACCAACATATGACGACCAAGGAGGACCGCTTCCAAATCCG 1281  
QY 1268 TTCCGCGATCGGAAACCCAGGTAAACACCCATTACAGAGAACACCCCTGCGCACAG 1327  
Db 1282 TTCCAGAACCCGAGCGAGGTCAACACCTTGTTCAGGCATCGCACCGGTCGACACT 1341  
QY 1328 CAGATTACCGCGATGCTTTTCTAGCGTCCGCTCGTCTGAGGTGGACTCTCGGTGTC 1387  
|||||

Db 1342 CAGATTACCGCGGATGCGTTAGTTACGGCGCGTGCAGCAAAACCATCGACTCAGCTC 1401  
QY 1388 ATGCTGACCTGGCGTGTGCGCAACACCGACCTGAAGCAAAACACTTTTGGTTTC 1447  
Db 1402 ATGCTGACCTGGCGTGTGCGCGCGGAGGCAAGAGGAGAGAACACTCTGGTTC 1461  
QY 1448 CAGAACATGTTCAAGACGGGTACAGTATGCCGCGAGCGAGTTCAGATATCGACCCAGC 1507  
Db 1462 TCGGACAAAATACGGACAGTACAAACATGCCGAGCGAGCTTCGACTTCGCTCCG 1521  
QY 1508 ACTG---CGTCAACAGTGAGAGCAAGAAATGATGCCCATATGTGCGAGTGGCGAGC 1564  
Db 1522 GCGGCGCGACGAGCAAGGAGGCGGAGCATGATGACCGATATGTGCTTATGTCGCG 1581  
QY 1565 AACTTGGAGGTATTATTGCCACGCTCCCGCGAGTTTATGGATCCAGGCTTGCACAT 1624  
Db 1582 AAGATTGGTGGCTTCTGCGCGCTCCCTCCGCAATTCATGAGCCCGGTCTTGTCTT 1641  
QY 1625 CATCTTGGGGGACTACTCGCATTTGGCTTCGAC-----AAGCAACTACAGTGGCTGAT 1678  
Db 1642 CACCTGGTGTACGACCGCATGGCTTCGAGGAGGAGGACAAGTGTGGTCAAC 1701  
QY 1679 AACAACTCGCTGCTGGGACTTTGCCAATCTTATGTTTGCAGCAATGSCACCATCAGG 1738  
Db 1702 ACGGACTCGCGCTGTTGGCTTCAAGAACTTCTCTCGGTGGCTCGGAAACATTC 1761  
QY 1739 ACGGGCTTGGCGGAGAACCGACACTTACGTCGATGTGCCACGCTATCAAGAGCGCGAG 1798  
Db 1762 ACGCGTACGCGGAAACCGAGCTCACCGCAATGTCCGTAATGTCTCGGATCAAGAGTTCGGAG 1821  
QY 1799 AGATCATCAATACATCA 1817  
Db 1822 TACATCAAGAACAATTCA 1840

RESULT 5  
AAZ46411  
ID AAZ46411 standard; DNA; 1902 BP.  
XX AC AAZ46411;  
XX DT 07-MAR-2000 (first entry)  
XX DE Pleurotus cornuoplae antitumour protein coding sequence.  
XX Antitumour; cancer; tumour; treatment; expression; tumour suppressor;  
KW p53; pBR; ss.  
XX OS Pleurotus cornuoplae.  
XX PN JP11315096-A.  
XX PD 16-NOV-1999.  
XX PF 07-AUG-1998; 98JP-0236349.  
XX PR 08-AUG-1997; 97JP-0215311.  
XX PR 02-MAR-1998; 98JP-0066176.  
XX (NEWF-) NEW FOOD CREATION GIJUTSU KENKYU KUMIAI.  
XX WPI; 2000-058170/05.  
XX P-PSDB; AAY52700.  
XX An antitumour protein derived from Pleurotus cornuoplae and its gene -  
XX useful for treatment of cancer including those caused by abnormal  
XX expression of cancer inhibitory gene (e.g. p53 and pBR)  
XX Claim 9; Page 15-16; 23pp; Japanese.  
XX The invention relates to a novel antitumour protein extracted from  
XX fruiting bodies of the fungus Pleurotus cornuoplae. The protein and  
XX nucleotides encoding it are useful for the treatment of cancer,





QY 1739 ACGGGCTTGGCGGAGAACCCGACACTTACGTCGATGTCGACGATCAAGAGCGCGAGG 1798  
Db 1612 GATCGGACTGCTGCAACCGGACTCGTACGAGCGTCGCTATGCGCTCAAGGGTGCTGAG 1671  
QY 1799 AGCATCATCAATCACT 1815  
Db 1672 GCTGTAGTCAATCACT 1688

RESULT 7  
AAA71487  
ID AAA71487 standard; cDNA; 1946 BP.  
XX  
AC AAA71487;  
XX  
DT 11-DEC-2000 (first entry)  
XX  
XX T. matsutake pyranose oxidase cDNA.  
XX  
DE Pyranose oxidase; matsutake mushroom; antibacterial; sugar metabolism;  
KW diabetes mellitus; ss.  
KW Tricholoma matsutake.  
XX

Key Location/Qualifiers  
CDS 101..1795  
FT /tag= a  
FT /product= "pyranose oxidase"  
XX JP2000175698-A.  
XX  
XX 27-JUN-2000.  
XX  
XX 16-DEC-1998; 98JP-0357423.  
XX  
XX 16-DEC-1998; 98JP-0357423.  
XX  
XX (NISR ) JAPAN TOBACCO INC.  
XX  
XX WPI; 2000-478485/42.  
XX  
XX P-PSDB; AAB10457.  
XX

A reagent containing pyranose oxidase for the determination of pyranose  
Disclosure; Page 14-17; 23pp; Japanese.  
XX  
XX This invention describes a novel reagent containing pyranose oxidase for  
XX the determination of pyranose which can be prepared from a fraction  
XX precipitated from an aqueous extract of matsutake mushroom by ammonium  
XX sulfate precipitation and has an antibacterial activity against at least  
XX Pyricularia oryzae or Thanatephorus cucumeris and has a M.W. of ca.  
XX 210 kD by gel filtration and shows the presence of components of ca.  
XX 50 kD and ca. 15 kD by SDS-PAGE and maintains the above antibacterial  
XX activity by being heated at 60 degrees C for 10 minutes in a neutral  
XX aqueous solution and in which the above antibacterial activity is  
XX inactivated by being heated at 80 degrees C for 10 minutes in a neutral  
XX aqueous solution. The invention also describes a method for the  
XX determination of pyranose in a sample in which the above reagent for the  
XX determination of pyranose is reacted with pyranose in the sample and the  
XX hydrogen peroxide formed is reacted with pyranose in the sample and the  
XX method for diagnosing a disease accompanied by abnormality in  
XX metabolism in which the above reagent for the determination of pyranose  
XX is reacted with pyranose in the sample and the hydrogen peroxide formed  
XX is reacted with an enzyme to develop a color, and a kit for pyranose  
XX analysis or the diagnosis of a disease accompanied by abnormality in  
XX sugar metabolism. The pyranose oxidase can be used as a diagnostic agent  
XX for diabetes mellitus. This sequence encodes the Tricholoma matsutake  
XX pyranose oxidase protein which is described in the method of the  
XX invention.  
XX  
XX Sequence 1946 BP; 484 A; 516 C; 475 G; 471 T; 0 other;

Query Match 6.1%; Score 129; DB 21; Length 1946;  
Best Local Similarity 52.5%; Pred. No. 6.1e-12;  
Matches 387; Conservative 0; Mismatches 305; Indels 45; Gaps 3;  
QY 1106 CTGGGAGGTACATACGAGACCGGATGCGATCTTTGCCAGATAGTCTTGAAGCAGGAA 1165  
Db 1064 CTTGGTGGCTACCTCAGGAACAGTCCATGACTTTTTTGTCTAGATTTCTCAAGAGGAGC 1123  
QY 1166 TTGTCGACAGCGTGGCGGAGGATCCTTTATGGACTGCGATGCGATGCGATGCGATGCGT 1225  
Db 1124 ATAGTCGATTCCATCGCTACTGACCCCT-----CGCTTCGCTGCGAAGGTTGAG 1171  
QY 1226 CAACATATTGCCAAGAACCGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1285  
Db 1172 GCGCACAGAGAGAGACCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231  
QY 1286 CAGGTAAACACCCATTTACAGAAACACCCCTGGCACGACGATTCACCGGATGCT 1345  
Db 1232 CAAGTGTATGATTCGCTACAGCTGCGACTTCCCTTGGCATGTTTCAGTCCATCGCTATGCA 1291  
QY 1346 TTTTCGTACGCTGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1405  
Db 1292 TTT-----GGTGTGTTGGACCCCAAGCGCGGCTGTTGCTGCTGCTGCTGCTGCTGCT 1345  
QY 1406 TTTGGCGCAACCGACCTGAAACAAACACCTTTTGGTTTTC----- 1448  
Db 1346 TTGGGCAATCAGATATTGTCGAAGAAATCGAGTGACTTTGGTCCGACCCCTAAGCTA 1405  
QY 1449 -----AGAACATGTTCAAGAGCGGTACAGTATGCCGACGCGGATTCAGATAT 1498  
Db 1406 CGCGACTGGGAGCGGGTGTACAGACACTTATGGAATGCCACAGCGGATTCATGCTC 1465  
QY 1499 CGACCCAGCACTCGCTCAACGCTGAGAGCAAGAAATGATGCGCGGATATGTCGGAAGTG 1558  
Db 1466 AAGCGGACCAACCGCGATGGAGACCGCTGACGAGGATGATGATGATGATGATGATGATGAT 1525  
QY 1559 GCGAGCAACTTGGGAGGTTATTGTCACACGTCCTCCCGCGAGTTTATGATCCAGGCTT 1618  
Db 1526 GCGACATAGTGGCGGGTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1585  
QY 1619 GCATCTATCTTGGCGGGTACTCTGATTCGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1678  
Db 1586 GCACAGCACATACGCGGAATCTACTCGGATCGGACAGATGATCAAACTTCTGTTGCTGAT 1645  
QY 1679 AACACTCGCTGCTGGGACTTTGCCAATCTTTATGTTGTCAGGCAATGCGACCATCAGG 1738  
Db 1646 CCGACATCAAGGTTTCAATCTGTCGACAACTCTGTTGGTGGCGGGAATGGTGCTATCCA 1705  
QY 1739 ACGGGCTTGGCGGAGAACCGGACACTTACGTCGATGTCGACGCTATCAAGAGCGCGAGG 1798  
Db 1706 GATGCGACTGCTGCAACCGGACTCGTACGAGGCTCGGCTATCGGCTTAAGGCTGCTGAG 1765  
QY 1799 AGCATCATCAATCACT 1815  
Db 1766 GCTGTAGTCACTTACT 1782  
RESULT 8  
AAA07403  
ID AAA07403 standard; DNA; 1946 BP.  
XX  
AC AAA07403;  
XX  
DT 07-JUL-2000 (first entry)  
XX  
XX Trichoderma derived antifungal protein coding sequence.  
XX  
DE Antifungal protein; Pyricularia oryzae; Rhizoctonia solani; mushroom;  
KW growth inhibitor; plant pathogenic fungi; antibacterial agent;  
KW N-terminal fragment; ss.  
XX  
XX Trichoderma matsutake.  
XX  
XX



W0200014242-A1.  
 16-MAR-2000.  
 19-AUG-1999; 99WO-JP04441.  
 08-SEP-1998; 98JP-0270606.  
 (NISR ) JAPAN TOBACCO INC.  
 (NORU ) SOC TECHNO-INNOVATION AGRIC FORESTRY & FI.  
 Takakura Y, Kuwata S, Ohta S;  
 WPI; 2000-256990/22.  
 P-PSDB; AAY81952.  
 Mushroom-derived antibacterial protein against plant pathogenic fungi  
 of rice; with activity and thermal stability, obtainable cheaply on  
 large scale, useful in agriculture  
 Claim 13; Page 41-45; 52pp; Japanese.  
 This sequence encodes the Trichoderma matsutake antibacterial protein of  
 the invention. The protein has activity against at least Pyricularia  
 oryzae and Rhizoctonia solani, and is obtained from a fraction of an  
 aqueous extract of a mushroom precipitated by the ammonium sulphate  
 precipitation method. The protein has a molecular weight of about 210 kD  
 as determined by the gel filtration method, includes components of about  
 15 kD and 50 kD in SDS-PAGE, and is stable to heating in an aqueous  
 neutral solution at 60 degrees C for 10 minutes but with loss of  
 antibacterial activity after heating in the solution at 80 degrees C for  
 10 minutes. The protein is used for inhibiting the growth of plant  
 pathogenic fungi e.g. Pyricularia oryzae and Rhizoctonia solani.  
 It is useful in treating rice plants, and is applicable in agriculture as  
 an antibacterial agent. The protein has activity at relatively low  
 concentrations, and can be produced at low cost on large scale.  
 Sequence 1946 BP; 484 A; 516 G; 475 G; 471 T; 0 other;  
 Query Match 6.1%; Score 129; DB 21; Length 1946;  
 Best Local Similarity 52.5%; Pred. No. 6.1e-12;  
 Matches 387; Conservative 0; Mismatches 305; Indels 45; Gaps 3;  
 QY 1106 CTGGGGAGGTACATACGGAGACCGATGGCATTTTGCAGATAGTCTTGAGGACAGAA 1165  
 Db 1064 CTTGGTCGTACTCTCAGCAAGTGCATGACATTTTGTGCAGATTGTTCTCAAGAGGAGC 1123  
 QY 1166 TTCTGTGACAGCTGCGGACGATCTTATGGACTGCCATGGTGGAAAGACGGCTTGC 1225  
 Db 1124 ATAGTCGATTCCTATCGCTACTGACCT-----CGCTTCGCTCGAAGGTTGAG 1171  
 QY 1226 CAACATATTGCCAAGAACCCGACAGATGCATGCCATTCGTTCCGCGATCCGGAACCC 1285  
 Db 1172 GCGCACAAAGAGACGCCCGATGAGCTGCTCCGATCCATCCACGAGCTGAACCT 1331  
 QY 1286 CAGGTAAACACCCCAATTTACAGAAGAACCCCTGGCACACGAGATTCACCGCGATGCT 1345  
 Db 1232 CAAGTGATGATTCGATACAGCTCGGACTTCCTTTGGCATGTTCCAGGTCCATCGCTATGCA 1291  
 QY 1346 TTTTCGTAGCTGCGCTGCTGAGTGGGACTCTCGTGTCATCTGTCGACCTGCGCTGG 1405  
 Db 1292 TTT-----GGTGATTTGGACCAAGGGCGGACCCCGCTGTTGCTGCTGATCTGAGGTTT 1345  
 QY 1406 TTTGGCGCAACCGACCTGAAGCAAAACACCTTTTGGTTTTC----- 1448  
 Db 1346 TTTCGCAATCAGATATTCTGNAGAAATCAGTACATTCCTCGTCCGAACCTAAGCTA 1405  
 QY 1449 -----AGAACGATGTTCAAGACGGGTACAGATATGCCGACGCGACGTTTCAGATAT 1498  
 Db 1406 CGCGACTGGAAAGCGGCTGTACAGACACTTATGGAATGCCACAGCCGACATTCATGTC 1465  
 QY 1499 CGACCCAGCACTGCTCAACAGTGTAGAGCAAGAAATGATGCGCGATATGTCGGAAGTG 1558

PR 25-APR-2000; 2000US-199654P.  
 PR 03-MAY-2000; 2000US-201516P.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 05-JUN-2000; 2000US-209832P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2001-602746/68.  
 P-PSDB; AAU29061.  
 XX  
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds  
 XX  
 PS Claim 2; Fig 75; 774pp; English.  
 XX  
 CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
 CC primers for PRO polypeptides of the invention. The sequences of the  
 CC invention can be used to detect the presence of a tumour in a mammal by  
 CC comparing the level of expression of a PRO polypeptide in a test sample  
 CC of cells from the animal and a control sample of normal cells, whereby a  
 CC higher level of expression in the test sample indicates the presence of a  
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
 CC blood when contacted with it. A specific polypeptide can be used to  
 CC stimulate the proliferation or differentiation of chondrocyte cells. The  
 CC PRO proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.  
 XX  
 SQ Sequence 4639 BP; 1426 A; 956 C; 1025 G; 1232 T; 0 other;

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 Db 4483 CAGTATCTTTTAAATGAGTCTTAAAAATAAGGCATATGTTTCATGTTTAAAAA 4542  
 QY 2039 AAAAAA 2106  
 Db 4543 AAAAAA 4610  
 QY 2099 AAAAAA 2106  
 Db 4603 AAAAAA 4610

RESULT 10  
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 ID AAC78483 standard; cDNA; 4640 BP.  
 XX  
 AC AAC78483;

XX 08-FEB-2001 (first entry)  
 XX Human PRO708 (UNQ372) nucleotide sequence SEQ ID NO:113.  
 DE Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;  
 XX expressed sequence tag; detection; cancer; ss.  
 KW Homo sapiens.  
 OS WO2000053756-A2.  
 XX  
 PN 14-SEP-2000.  
 XX  
 PD 18-FEB-2000; 2000WO-US04341.  
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 PF 08-MAR-1999; 99WO-US05028.  
 XX 12-MAR-1999; 99US-0123957.  
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 PR 06-JAN-2000; 2000WO-US00219.  
 PR 08-JAN-2000; 2000WO-US00277.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX WPI: 2000-611443/58.  
 DR P-PSDB; AAB44257.  
 XX  
 XX Novel PRO polypeptides and polynucleotides used in detection methods,  
 PT to target bioactive molecules to specific cells, and to modulate  
 PT cellular activities  
 XX  
 PS Claim 2; Fig 42; 636pp; English.  
 XX  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO  
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.  
 XX  
 SQ Sequence 4640 BP; 1427 A; 955 C; 1026 G; 1232 T; 0 other;

Query Match 4.5%; Score 94.4; DB 21; Length 4640;  
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 Db 4423 TATGGCTCCATTTATTTATAGTGTAAAGTTGTATTTCTTAAAGTTTGTGTTCGA 4482

RESULT 10  
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 ID AAC78483 standard; cDNA; 4640 BP.  
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 AC AAC78483;

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RESULT 11
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XX
AC  ACAS7720;
XX
DT  10-JUN-2003 (first entry)
DE  Human PRO708 cDNA.
XX
KW  * Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood; gene;
KW  tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW  differentiation; tumour; gene therapy; ss.
XX
OS  Homo sapiens.
XX
PN  US2003036143-A1.
XX
PD  20-FEB-2003.
XX
PF  02-JUL-2002; 2002US-0187600.
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Matches 137; Conservative 0; Mismatches 46; Indels 5; Gaps 1;

QY 1924 TCTGGTCCCTACCATGTTGATGTGACGATAGCGCTGGAAGATTTGTGTATTACTGA 1983
Db 4423 TATGGCTCCATTTATTTATAGTGAAGTTGTATTTCTTAAGTTTGTGTTTCTCGA 4482
QY 1984 ACTGTACTTGTCTGA-----ATAGTTATGGCAGCATGATTTTAAAGAAAAA 2038
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Db 4543 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4602
QY 2099 AAAAAAAA 2106
Db 4603 AAAAAAAA 4610

RESULT 13
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AC ABX98692;
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DT 20-MAY-2003 (first entry)
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KW Human; secreted protein; transmembrane protein; cytosolic;
KW gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036157-A1.
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PD 20-FEB-2003.
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PF 02-JUL-2002; 2002US-0188769.
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PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
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PR 05-JAN-2000; 2000WO-US00219.
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